

SEQUENCE LISTING

<110> Pasamontes, Luis
Tsygankov, Yuri

<120> Fermentative Carotenoid Production

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<140> 09/920,923
<141> 2001-08-02

<150> 08/980,832
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<170> PatentIn version 3.1

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Val Leu Met Leu Met Val Ala Glu Ser Ser Gly Gly Val Cys Asp Ala
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Met Val Asp Ala Ala Cys Ala Val Glu Met Val His Ala Ala Ser Leu
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Ile Phe Asp Asp Met Pro Cys Met Asp Asp Ala Arg Thr Arg Arg Gly
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Gln Pro Ala Thr His Val Ala His Gly Glu Gly Arg Ala Val Leu Ala
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Ala Met Gly Pro Val Gly Leu Cys Ala Gly Gln Asp Leu Asp Leu His
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Ala Pro Lys Asp Ala Ala Gly Ile Glu Arg Glu Gln Asp Leu Lys Thr
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Gly Val Leu Phe Val Ala Gly Leu Glu Met Leu Ser Ile Ile Lys Gly
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Leu Asp Lys Ala Glu Thr Glu Gln Leu Met Ala Phe Gly Arg Gln Leu
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Gly Arg Val Phe Gln Ser Tyr Asp Asp Leu Leu Asp Val Ile Gly Asp
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Lys Ala Ser Thr Gly Lys Asp Thr Ala Arg Asp Thr Ala Ala Pro Gly
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Pro Lys Gly Gly Leu Met Ala Val Gly Gln Met Gly Asp Val Ala Gln
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His Tyr Arg Ala Ser Arg Ala Gln Leu Asp Glu Leu Met Arg Thr Arg
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Ala Arg Leu Gly Ala Leu Arg Ala Asp Thr Leu Ala Ala Leu His Glu
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Asp Gly Pro Met Ser Pro Pro Phe Ala Ala Leu Arg Gln Val Ala Arg
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Arg His Asp Phe Pro Asp Leu Trp Pro Met Asp Leu Ile Glu Gly Phe
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Glu Tyr Ser Tyr His Val Ala Gly Val Val Gly Val Met Met Ala Arg
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Val Met Gly Val Gln Asp Asp Ala Val Leu Asp Arg Ala Cys Asp Leu
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Ala Ala Ile Gly Arg Cys Tyr Leu Pro Ala Asp Trp Leu Ala Glu Ala
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Ile Ile Arg Leu Leu Asp Ala Ala Glu Pro Tyr Tyr Ala Ser Ala Arg
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Ala Leu Arg Ile Tyr Arg Ala Ile Gly Thr Arg Ile Arg Gln Gly Gly
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Pro Glu Ala Tyr Arg Gln Arg Ile Ser Thr Ser Lys Ala Ala Lys Ile
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Glu Glu Val Tyr Arg Glu Gly Tyr Leu Lys Leu Gly Thr Thr Pro Phe
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Pro His Leu Arg Gln Ala Phe Ser Phe His Thr Leu Leu Val Gly Gly
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Arg Arg Gly Gly Val Trp Phe Ala Lys Gly Gly Thr Asn Gln Leu Val
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Thr His Tyr Val Leu Ala Pro Val Pro His Leu Gly Arg Ala Asp Val
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Arg Ile Phe Ser Pro Ala Asp Phe Ser Thr Glu Leu Ser Ala His His
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Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
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Arg Pro His Asn Arg Asp Arg Ala Ile Pro Asn Phe Tyr Ile Val Gly
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Asp Thr Asp Leu Ser Pro Glu Trp Leu Ala Arg Leu Ser Pro Ile Arg
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Arg Gly Glu Trp Thr Asp Gln Glu Val Ala Phe Pro Asp His Ser Arg
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Arg Leu Thr Thr Gly Tyr Gly Ser Ile Glu Ala Gly Ala Leu Ile Gly
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Cys Val Ile Asp Ala Arg Gly Ala Val Glu Thr Pro His Leu Thr Val
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<210> 28
 <211> 726
 <212> DNA
 <213> Alcaligenes PC-1

<400> 28
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 gctgctatcg gtcagctggc tctgtggctg tacgctgggt tctcctggcc gaaactgata 300
 gctaaacaca tgaccacca ccgtcacgct ggtaccgaca acgaccgga cttcgggtcac 360
 ggtgggtcgg ttctgttgga cggttccttc gtttccacct acttcgggtg gcgtgaagg 420
 ctgctgctgc cggttatcgt taccacctac gctctgatcc tgggtgaccg ttggatgtac 480
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 ggtatcgggtg acccgctgct cctgctgacc tgcttccact tcggtgggta ccaccacgaa 660
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 cgtgct 726

<210> 29
 <211> 242
 <212> PRT
 <213> Alcaligenes PC-1

<400> 29

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Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
225 230 235 240

Arg Ala

<210> 30
<211> 1261
<212> DNA
<213> *Alcaligenes* PC-1

<400> 30
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gccctgcatg tgcatgcgct gtggtttctg gacgcggcgg cgcattccat cctggcggtc 180
gcgaatttcc tggggctgac ctggctgtcg gtcggctctgt tcatcatcgc gcatgacgcg 240
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ctgtggctgt atgccggatt ttcctggcgc aagatgatcg tcaagcacat ggcccatcat 360
cgccatgccg gaaccgacga cgaccagat ttcgaccatg gcggcccggg ccgctggtac 420
gcccgttca tcggcaccta tttcggctgg cgcgaggggc tgetgctgcc cgtcatcgtg 480
acggtctatg cgctgatgtt gggggatcgc tggatgtacg tgggtttctg gccgttgccg 540
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cacgacgcgt tcccggaccg ccacaatgcg cggctcgtcg ggatcagcga ccccggtgctg 660
ctgctgacct gctttcactt tggcggttat catcacgaac accacctgca cccgacgggtg 720
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tcgtcgtcgc caccgtgctg gtgatggagc tgacggccta ttccgtccac cgctggatca 840
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tgaaaaagaa cgacctgtac ggctgtgtct ttgcggtgat cgccacgggtg ctgttcacgg 960
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ggcgcgacca ttgcgtcagc ttcggcttca tctatgcgcc gccggtcgac aagctgaagc 1200
aggacctgaa gacgtcgggc gtgctgcggg ccgaggcgca ggagcgcacg tgacctatga 1260
c 1261

<210> 31

<211> 729
 <212> DNA
 <213> Unknown

<220>
 <223> E-396

<400> 31
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 gcgcacatccca tcctggcggt cgccaatttc ctggggctga cctggctgtc ggtcggctcg 180
 ttcatcatcg cgcacatgacgc gatgcatggg tcggctcgtgc cggggcgccc gcgcgccaat 240
 gcggcgatgg gccagcttgt cctgtggctg tatgccggat tttcctggcg caagatgac 300
 gtcaagcaca tggcccatca tcgccatgcc ggaaccgacg acgaccaga tttcgacat 360
 ggcgggcccg tccgctggta cgcccgcttc atcggaacct atttcggctg gcgcgagggg 420
 ctgctcgtgc ccgtcatcgt gacggctctat gcgctgatgt tgggggatcg ctggatgtac 480
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 tggctgccgc accgccccgg ccacgacgcg ttcccgacc gccacaatgc gcggtcgtcg 600
 cggatcagcg accccgtgtc gctgctgacc tgctttcaact ttggcgggta tcatcacgaa 660
 caccacctgc acccgacggt gccttggtgg cgctgccca gcacccgcac caagggggac 720
 accgcatga 729

<210> 32
 <211> 242
 <212> PRT
 <213> Unknown

<220>
 <223> E-396

<400> 32

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
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Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Met Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Ile Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

Thr Ala

<210> 33
 <211> 486
 <212> DNA
 <213> Unknown

<220>

<223> E-396

<400> 33

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gtccaccgct ggatcatgca cggcccccttg ggctggggct ggcacaagtc ccaccacgag      120
gaacacgacc acgcgctgga aaagaacgac ctgtacggcc tggctctttgc ggtgatcgcc      180
acggtgctgt tcacggtggg ctggatctgg gcaccgggcc tgtggtggat cgccttgggc      240
atgaccgtct acgggctgat ctatttcgtc ctgcatgacg ggctggtgca tcagcgctgg      300
cogttccgct atatccctcg caagggctat gccagacgcc tgtatcaggc ccaccgcctg      360
caccacgcgg tcgagggggcg cgaccattgc gtcagcttcg gcttcatcta tgcgccgccg      420
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cgcacg                                         486
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<210> 34

<211> 162

<212> PRT

<213> Unknown

<220>

<223> E-396

<400> 34

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Met Thr Asn Phe Leu Ile Val Val Ala Thr Val Leu Val Met Glu Leu
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Thr Ala Tyr Ser Val His Arg Trp Ile Met His Gly Pro Leu Gly Trp
                20              25              30

Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys
                35              40              45

Asn Asp Leu Tyr Gly Leu Val Phe Ala Val Ile Ala Thr Val Leu Phe
50              55              60

Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly
65              70              75              80

Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val
                85              90              95
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His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg
 100 105 110

Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
 115 120 125

His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
 130 135 140

Lys Gln Asp Leu Lys Thr Ser Gly Val Leu Arg Ala Glu Ala Gln Glu
 145 150 155 160

Arg Thr

<210> 35
 <211> 1253
 <212> DNA
 <213> Unknown

<220>
 <223> E-396

<220>
 <221> misc_feature
 <222> (911)..(911)
 <223> unsure

<400> 35
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 gaacaccccg cccagctgac ggccaaagtc gatcatctga gtctgctcct cggcgtcgaa 180
 ctctttgatc acggccagca tctccagccc ggcgatgaac agcacgcccg tcttcaggtc 240
 ctgtttcctgt tcgacccccg cgccgttctt ggccgcgtgc aggtccaggt cctggccggc 300
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 gcccgacgcg ccgcgcgcac cggccagcag ggccatcgcc tcggtgatca gggcgatgcc 420
 gcctagcacg gcgcggcttt cgccatgcgc cacatgggtc gcgggctggc cgcggcgcac 480
 cccggcatcg tccatgcagg gcaggctcgc gaagatcagc gatgcggcat gcaccatctc 540
 gaccgcgcag gcggcgtcga cgatcgtgtc gcagaccccg cccgaggctt ctgccgcaag 600
 cagcatcagc atgccgcgga aacgcttgcc cgacgacagc gcgccatggc tcatggccgg 660

gccgagcggc tgcgacacgg caccgaatcc ctgggcgatc tcctcaagtc tggctctgcag 720
 aaggggtggcg tggatcgggt tgacgtctcg tctcatcagt gccttcgcgc ttgggttctg 780
 accaggcggg aaggtcaggc cggggcgga ccccgtagc cgtcatccac cgtcaacagt 840
 ccccatgttg gaaggcttca cgcccgattg cgagcctttt cgacggcgac gcgggggtcgc 900
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 atccttggcc ggaacacccc gcgcgcgc atgatcggcc aggatcgtcc ggcgcgcggc 1020
 gcggcgagc tggcgccgt caccggatt gtcaagcacc caggccatcg cgtccgcgac 1080
 ctgctccgcg tctccatgt cgacgatcag gccgttctcc atgtcgcgga ccagttcgcg 1140
 caccggggcg gtgttcgatc gatcaccagg catccggtgg ccatcgctc ggacagggac 1200
 caggaggtga cgaagggtc ggtgaaatag acatgcgcgt gcgaggcctg cag 1253

<210> 36
 <211> 882
 <212> DNA
 <213> Unknown

<220>
 <223> E-396

<400> 36
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 gccagggat tgggtgccgt gtcgcagccg ctgggcccg ccatgagcca tggcgcgctg 120
 tctcgggca agcgtttccg cggcatgctg atgtgcttg cggcagaagc ctggggcggg 180
 gtctgcgaca cgatcgtcga cgccgcctgc gcggtcgaga tgggtgcatgc cgcacgctg 240
 atcttcgacg acctgccctg catggacgat gccgggctgc gccgcggcca gcccgcgacc 300
 catgtggcgc atggcgaaag ccgcgccgtg ctaggcgga tgcacctgat caccgaggcg 360
 atggccctgc tggccggtgc gcgcggcgcg tcgggcacgg tgcgggcgca gctgggtgcg 420
 atcctgtcgc ggtccctggg gccgcagggc ctgtgcgcgc gccaggacct ggacctgcac 480
 gcggccaaga acggcgcggg ggtcgaacag gaacaggacc tgaagaccg cgtgctgttc 540
 atcgccgggc tggagatgct ggccgtgatc aaggagtctg acgccagga gcagactcag 600
 atgatcgact ttggccgtca gctgggcccgtgttccagt cctatgacga cctgctggac 660
 gttgtgggcg accaggcggc gcttggcaag gataccggtc gcgatgcggc ggcccccggc 720
 ccgcggcgcg gccttctggc cgtgtcagac ctgcagaacg tgtcccgta ctatgaggcc 780
 agccgcgccc agctggacgc gatgctgcgc agcaagcgc ttcaggctcc ggaaatcgcg 840

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<210> 37
<211> 293
<212> PRT
<213> Unknown

<220>
<223> E-396

<400> 37

Met Arg Arg Asp Val Asn Pro Ile His Ala Thr Leu Leu Gln Thr Arg
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Leu Glu Glu Ile Ala Gln Gly Phe Gly Ala Val Ser Gln Pro Leu Gly
20 25 30

Pro Ala Met Ser His Gly Ala Leu Ser Ser Gly Lys Arg Phe Arg Gly
35 40 45

Met Leu Met Leu Leu Ala Ala Glu Ala Ser Gly Gly Val Cys Asp Thr
50 55 60

Ile Val Asp Ala Ala Cys Ala Val Glu Met Val His Ala Ala Ser Leu
65 70 75 80

Ile Phe Asp Asp Leu Pro Cys Met Asp Asp Ala Gly Leu Arg Arg Gly
85 90 95

Gln Pro Ala Thr His Val Ala His Gly Glu Ser Arg Ala Val Leu Gly
100 105 110

Gly Ile Ala Leu Ile Thr Glu Ala Met Ala Leu Leu Ala Gly Ala Arg
115 120 125

Gly Ala Ser Gly Thr Val Arg Ala Gln Leu Val Arg Ile Leu Ser Arg
130 135 140

Ser Leu Gly Pro Gln Gly Leu Cys Ala Gly Gln Asp Leu Asp Leu His
145 150 155 160

Ala Ala Lys Asn Gly Ala Gly Val Glu Gln Glu Gln Asp Leu Lys Thr
165 170 175

Gly Val Leu Phe Ile Ala Gly Leu Glu Met Leu Ala Val Ile Lys Glu
 180 185 190

Phe Asp Ala Glu Glu Gln Thr Gln Met Ile Asp Phe Gly Arg Gln Leu
 195 200 205

Gly Arg Val Phe Gln Ser Tyr Asp Asp Leu Leu Asp Val Val Gly Asp
 210 215 220

Gln Ala Ala Leu Gly Lys Asp Thr Gly Arg Asp Ala Ala Ala Pro Gly
 225 230 235 240

Pro Arg Arg Gly Leu Leu Ala Val Ser Asp Leu Gln Asn Val Ser Arg
 245 250 255

His Tyr Glu Ala Ser Arg Ala Gln Leu Asp Ala Met Leu Arg Ser Lys
 260 265 270

Arg Leu Gln Ala Pro Glu Ile Ala Ala Leu Leu Glu Arg Val Leu Pro
 275 280 285

Tyr Ala Ala Arg Ala
 290

<210> 38
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> Primer #7

<400> 38
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25

<210> 39
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> Primer #8

<400> 39
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20

<210> 40
 <211> 391
 <212> PRT
 <213> Flavobacterium sp. R1534

<400> 40

Met Asp Pro Ile Val Ile Thr Gly Ala Met Arg Thr Pro Met Gly Ala
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Phe Gln Gly Asp Leu Ala Ala Met Asp Ala Pro Thr Leu Gly Ala Asp
 20 25 30

Ala Ile Arg Ala Ala Leu Asn Gly Leu Ser Pro Asp Met Val Asp Glu
 35 40 45

Val Leu Met Gly Cys Val Leu Ala Ala Gly Gln Gly Gln Ala Pro Ala
 50 55 60

Arg Gln Ala Ala Leu Gly Ala Gly Leu Pro Leu Ser Thr Gly Thr Thr
 65 70 75 80

Thr Ile Asn Glu Met Cys Gly Ser Gly Met Lys Ala Ala Met Leu Gly
 85 90 95

His Asp Leu Ile Ala Ala Gly Ser Ala Gly Ile Val Val Ala Gly Gly
 100 105 110

Met Glu Ser Met Ser Asn Ala Pro Tyr Leu Leu Pro Lys Ala Arg Ser
 115 120 125

Gly Met Arg Met Gly His Asp Arg Val Leu Asp His Met Phe Leu Asp
 130 135 140

Gly Leu Glu Asp Ala Tyr Asp Lys Gly Arg Leu Met Gly Thr Phe Ala
 145 150 155 160

Glu Asp Cys Ala Gly Asp His Gly Phe Thr Arg Glu Ala Gln Asp Asp
 165 170 175

Tyr Ala Leu Thr Ser Leu Ala Arg Ala Gln Asp Ala Ile Ala Ser Gly
 180 185 190

Ala Phe Ala Ala Glu Ile Ala Pro Val Thr Val Thr Ala Arg Lys Val
 195 200 205

Gln Thr Thr Val Asp Thr Asp Glu Met Pro Gly Lys Ala Arg Pro Glu
 210 215 220

Lys Ile Pro His Leu Lys Pro Ala Phe Arg Asp Gly Gly Thr Val Thr
 225 230 235 240

Ala Ala Asn Ser Ser Ser Ile Ser Asp Gly Ala Ala Ala Leu Val Met
 245 250 255

Met Arg Gln Ser Gln Ala Glu Lys Leu Gly Leu Thr Pro Ile Ala Arg
 260 265 270

Ile Ile Gly His Ala Thr His Ala Asp Arg Pro Gly Leu Phe Pro Thr
 275 280 285

Ala Pro Ile Gly Ala Met Arg Lys Leu Leu Asp Arg Thr Asp Thr Arg
 290 295 300

Leu Gly Asp Tyr Asp Leu Phe Glu Val Asn Glu Ala Phe Ala Val Val
 305 310 315 320

Ala Met Ile Ala Met Lys Glu Leu Gly Leu Pro His Asp Ala Thr Asn
 325 330 335

Ile Asn Gly Gly Ala Cys Ala Leu Gly His Pro Ile Gly Ala Ser Gly
 340 345 350

Ala Arg Ile Met Val Thr Leu Leu Asn Ala Met Ala Ala Arg Gly Ala
 355 360 365

Thr Arg Gly Ala Ala Ser Val Cys Ile Gly Gly Gly Glu Ala Thr Ala
 370 375 380

Ile Ala Leu Glu Arg Leu Ser
 385 390

<210> 41
 <211> 388
 <212> PRT
 <213> Flavobacterium sp. R1534
 <400> 41

Asp Pro Arg Leu Ala Val Arg Asp Gln Gln Pro Pro Leu Arg Ile Gly
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 Gln His His Pro His Glu Pro Gln Arg Thr Thr Gln Arg Ala Pro Gln
 20 25 30
 Ile Gly Arg Val Gln His Gly Met Arg His His Arg Glu Gly Pro Arg
 35 40 45
 Arg His Gly Ala Arg Ala His Ser Glu Glu Leu Ala Ala Cys Pro Leu
 50 55 60
 Arg Lys Val Ala Pro Asp Arg Ala Val Phe Arg Cys Ser Asp Gly Pro
 65 70 75 80
 Asp Ala Arg Gly Pro Ala Leu Pro Arg Arg His Gln Arg Ile Ala His
 85 90 95
 Glu Pro Phe Arg Asp Asp Val Leu Ile His Gly Pro Ser Leu Gln Asn
 100 105 110
 Arg Ser Pro Ile Leu Ser Arg Asp Gly Ile Val Cys Asn Ala Pro Arg
 115 120 125
 Ala Arg Met Ala Arg Arg Ile Lys Gly Gly Arg Asp Met Glu Ile Glu
 130 135 140
 Gly Arg Val Phe Val Val Thr Gly Ala Ala Ser Gly Leu Gly Ala Ala
 145 150 155 160
 Ser Ala Arg Met Leu Ala Gln Gly Gly Ala Lys Val Val Leu Ala Asp
 165 170 175
 Leu Ala Glu Pro Lys Asp Ala Pro Glu Gly Ala Val His Ala Ala Cys
 180 185 190
 Asp Val Thr Asp Ala Thr Ala Ala Gln Thr Ala Ile Ala Leu Ala Thr
 195 200 205
 Asp Arg Phe Gly Arg Leu Asp Gly Leu Val Asn Cys Ala Gly Ile Ala
 210 215 220

Pro Ala Glu Arg Met Leu Gly Arg Asp Gly Pro His Gly Leu Asp Ser
 225 230 235 240

Phe Ala Arg Ala Val Thr Ile Asn Leu Ile Gly Ser Phe Asn Met Ala
 245 250 255

Arg Leu Ala Ala Glu Ala Met Ala Arg Asn Glu Pro Val Arg Gly Glu
 260 265 270

Arg Gly Val Ile Val Asn Thr Ala Ser Ile Ala Ala Gln Asp Gly Gln
 275 280 285

Ile Gly Gln Val Ala Tyr Ala Ala Ser Lys Ala Gly Val Ala Gly Met
 290 295 300

Thr Leu Pro Met Ala Arg Asp Leu Ala Arg His Gly Ile Arg Val Met
 305 310 315 320

Thr Ile Ala Pro Gly Ile Phe Arg Thr Pro Met Leu Glu Gly Leu Pro
 325 330 335

Gln Asp Val Gln Asp Ser Leu Gly Ala Ala Val Pro Phe Pro Ser Arg
 340 345 350

Leu Gly Glu Pro Ser Glu Tyr Ala Ala Leu Leu His His Ile Ile Ala
 355 360 365

Asn Pro Met Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala Leu Arg
 370 375 380

Met Ala Pro Lys
 385

<210> 42
 <211> 182
 <212> PRT
 <213> Flavobacterium sp. R1534

<400> 42

Met Thr Gly Thr Arg Met Arg Arg Val Ser Arg Ile Ser Ala Pro Ser
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Ser Pro Ile Leu Pro Met Trp Pro Ser Lys Ala Ala Ala Leu Leu Ala
 20 25 30

Val Leu Met Pro Ala Ala Ala Ala Val Glu Cys Ala Pro Gly Ser
 35 40 45

Leu Val Val Asp Thr Gly Ala Glu Thr Leu Gly Phe Arg Val Glu Val
 50 55 60

Ala Asp Ser Pro Glu Glu Arg Ala Gln Gly Leu Met Phe Arg Lys Glu
 65 70 75 80

Leu Pro Ala Gly Thr Gly Met Leu Phe Ile Tyr Glu Ser Pro Gln Pro
 85 90 95

Val Ser Phe Trp Met Arg Asn Thr Leu Ile Pro Leu Asp Met Val Phe
 100 105 110

Ala Asp Glu Thr Gly Val Ile Arg His Ile His Arg Asn Ala Arg Pro
 115 120 125

Leu Asp Glu Thr Pro Ile Pro Gly Ala Ala Val Gly Asp Pro Asp Pro
 130 135 140

Asp Arg Leu Phe Val Leu Glu Ile Ala Gly Gly Glu Ala Asp Arg Leu
 145 150 155 160

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